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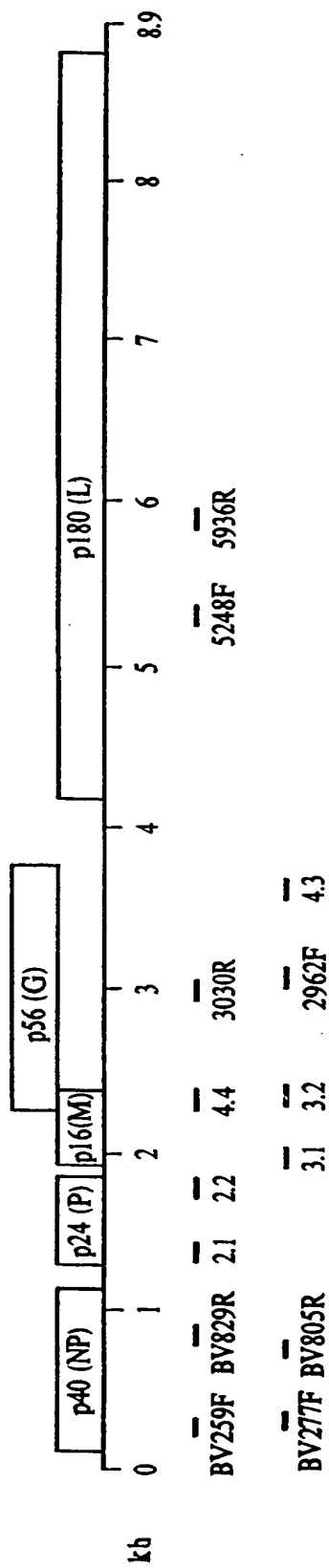


FIG. 1



Consensus	CTATAGATTGGATTAAACGGCCARCCCTGGGTAGGCTCCTTTGTGTGTTGTCTCTACTACTACAGACTTTTGAGTCCCCAGGTAAAGAATTYA	720
BDV JCTG.....	720
BDV BrieseA.....T.	720
Consensus	TGGAYCAGATTAAARCTTGTTCGCAAGTTATGCRACAGATGACTAGCTACACTATAAAGGAGTACCTCGCAGAATGYATGGATGCTACCC	810
BDV JCTT.....A.....G.....T.....	810
BDV BrieseC.....G.....A.....C.....	810
Consensus	TTACAATCCCCTAGTTCATATGAGATYCGTGACTTTTTAGAAGTTTCAGCAAGCTTAARGAGGAWCATGCTGACCTGTTTCGGTTTC	900
BDV JCTT.....T.....A.....T.....C.....	900
BDV BrieseC.....C.....G.....T.....C.....	900
Consensus	TGGGGGCGYATTMGRCACCCCGACGCTATCAAGCTKGGCCACGRAGCTTCCCAATCTGGCTCYGCAGCGTTTACTGGAGTAAAGAAGG	990
BDV JCTT...C.G.....T.....G.....T..T.....	990
BDV BrieseC...A.A.....G.....A.....C..C.....	990
Consensus	ARAYCCACAATGGCRGGCTACCGGGCCCTCCACCATCCAGCGGGCGGRAGTGTCAAGGARACCCAGCTGCCCGGTATAGGCCCGCGG	1080
BDV JCT	.G..T.....G.....G.....G.....	1080
BDV Briese	.A..C.....A.....A.....A.....	1080
Consensus	AGATATCTCGYGGRGARGACGGGCAGAGCTCTCAGGTGAGATCTCTGCCATAATGARRATCATAGGTGTGACTGGTCTAAACTARAAAA	1170
BDV JCTC..G..A.....GA.....G....	1170
BDV BrieseT..A..G.....AG.....A....	1170
Consensus	CAATGAACAAACCAATAAAAAACCAAAATGGCGCAACCCYCCGGACCTGYGATGAGYTCGGACCTCCGGCTGACATGCTTGAAYTAGT	1260
BDV JCTC.....T.....C.....C....	1260
BDV BrieseT.....C.....C.....C....	1260
Consensus	CAGGAGGCTCAATGGCAACGCGACCATCGAGTCTGGTGGACTCCCTCGAGGACGAGAGAGATCCCCAGACACTACGACGGGAACGAYCGG	1350
BDV JCTG.....T.....T....	1350
BDV BrieseC.....C.....C.....C....	1350

FIG. 2B

Consensus	GGTCACCAAGACCAAGGAGRTCCCAAGGAATGCATTGACCCACCRGTAGACAGCTCCTGAAGGACCTCAGGAAGAAACCCCTCCATGA	1440
BDV JCTA.....G.....	1440
BDV BrieseG.....A.....	1440
Consensus	TCTCAGACCCAGACGACCGAAGCGGAGCAGCTRTTCGAATGATGAGTWTATCAAGAAGYTAGTGACGGAGCTGGCGGAGAAATAGCA	1530
BDV JCTA.....T.....C.....	1530
BDV BrieseG.....A.....T.....	1530
Consensus	TGATCGAGGCTGAGGAGGTGCGGGGCACTCTTGGRGACATCTCGGCTCGYATCGAGGAGGGTTTGAGTCCCTGTCCGCCCTCCAAGTGG	1620
BDV JCTG.....C.....	1620
BDV BrieseA.....T.....	1620
Consensus	AAACCATCCAGACAGCTCAGCGGTGCGAYCACTCCGAYAGCATCAGRATCCTYGGGAGAACATCAAGATACTRGATCGTCCATGAAGA	1710
BDV JCTC.....T.....A.....T.....G.....	1710
BDV BrieseT.....C.....G.....C.....A.....	1710
Consensus	CAATGATGGAGACAATGAAGCTCATGATGGAGAGGTGGAYCTCCTCTAGGCATCAACCGCCGTTGGGACCTCTGCACCCATGTTGCCCT	1800
BDV JCTC.....	1800
BDV BrieseT.....	1800
Consensus	CCCATCCTGCACCTCCGGCATTTATCCCCAGCTCCCAAGTGCCCCGACARCGGATGARTGGGACATCATACCATAAAAAATCGAATCA	1890
BDV JCTG.....G.....	1890
BDV BrieseA.....A.....	1890
Consensus	CCATGAATTCAAARCATTCCTATGTGGAGCTCAAGRCAAGGTAATCGTCCCTGGATGCCCCACACTGATGCTTGAGATAGACTTTGTAG	1980
BDV JCTG.....	1980
BDV BrieseA.....	1980
Consensus	GRGGGACTTCACGGAACCAAGTTCCTTAACATCCCATTTCTTTTCAGTGAAGAGCCTCTGCAGCTTCCACGCGGAGAGAGTTGACCGACT	2070
BDV JCT	.A.....	2070
BDV Briese	.G.....	2070

FIG. 2C

Consensus	ACTTYACVATTGACGTAGARCCAGCAGGTCAATCCCTGGTCAAYATATACTTCCAGATTGACGACTTCTTGTCTCTCAACTCAACTCAC	2160
BDV JCT	...C..C.....G.....C.....	2160
BDV Briese	...T..T.....A.....T.....	2160
Consensus	TRTCYGRNTACAAGGACCCGATTAGRAAATACATGTTCTACGGCTCAACAAGGAMCAGAGCAAGCAGCAATYAATGCAGCYTTCAATG	2250
BDV JCT	.G..C..A.....G.....A.....	2250
BDV Briese	.A..T..G.....A.....C.....	2250
Consensus	TCTTYTCTTATCGGCTTCGGAACATTGGTGTGGYCCTCTCGGCCCGACATTCGATCTTCAGGGCCTTAGYTGCAATACTGACTCCACT	2340
BDV JCT	...C.....C.....T.....G.....	2340
BDV Briese	...T.....T.....G.....C.....	2340
Consensus	CCTGGAYTRATYGAICTGGAGATAAGGCGACTTGGCCACACCCCAACGGAAATGTCATTTTCATGCGAGGTTAGTTATCTCTYAACCACACG	2430
BDV JCTT.A..C..T.....G.....	2430
BDV BrieseC.G..T..C.....C.....	2430
Consensus	ACTATTAGCCTCCGGCAGTCCACACRATCATGCCTCAAGTACCACCTGCAAAACCTATTGGGGATTCTTTGGTAGCTACAGCGCTGACCGA	2520
BDV JCTG.....A.....	2520
BDV BrieseA.....	2520
Consensus	ATCATMAATCGGTACACTGGTACTGTTAAGGGTTGTGTAAACAACCTCAGCRCCAGAGAYCCCTTCGAGTGCAACTGGTTCTACTGCTGC	2610
BDV JCT	...C.....T.....G.....T.....	2610
BDV Briese	...A.....C.....A.....C.....	2610
Consensus	TGGCGGATTACAACAGAGATCTGCCGATGCTCTATTACAAATGTACGGTGGCTGTRCARACATTCACCAGTTTCATGTACTGCAGTTTY	2700
BDV JCTA..G.....C.....	2700
BDV BrieseG..A.....T.....	2700
Consensus	GCRGACTGYAGTACYGTGAGYCARCAGGAGCTAGAGAGTGGMAAGGCAATGCTGAGCGATGGCAGTACMTTACTTATACCCCGTATATC	2790
BDV JCT seq	..G....T....T....T..G.....C.....	2790
BDV Briese	..A.....C.....C.....A.....A.....	2790

FIG. 2D

Consensus BDV JCT BDV Briese	CAGCAGACACAGCCAAGAGCAGATGCCAYCTCCTAATCGCCTCAGTGGTCCARGGRGCCCTTTGGGARCAAGGTCATTCTTGTATCATAC.....A.A.....G.....T.....G.G.....A.....	4320 4320 4320
Consensus BDV JCT BDV Briese	TAATCAACATGATCGACAYAAATTGACTCAATCAACCTCCCCATGATGATTACTTCACAATTATTAAAGTCTATCTYTCCTACTCCCAAGC.....T.....	4410 4410 4410
Consensus BDV JCT BDV Briese	GGCTTGTTATGGGGAGGCAAYAATGTRTCAGTCTCCTCTGATTYGGTCCGTATTTRCYATTCTCTGAATYATGCCCRCAACTAGACAGCTC.....G.....T.....A.T.....C.....A.....T.....A.....C.....G.C.....T.....G.....	4500 4500 4500
Consensus BDV JCT BDV Briese	TACTAAAAAACTGCTYCAACTTGACCCYGTTCCTCCTCATGGTCTCTTCGGTGCAGAAGTCATGGTACTTCCTCAGATCCGAATGGT.....T.....C.....C.....	4590 4590 4590
Consensus BDV JCT BDV Briese	TYGACGGGTCACGGGAGCAGCTCCACAAGATGCGTGTGAGCTGGARAGCCCCCAGCCCTGCTGTCTAGGGCCATACCCCTCCTGTCAA .T.....G.....A..... .C.....A.....G.....	4680 4680 4680
Consensus BDV JCT BDV Briese	TATTCGRGCAGAGTTTATCAAGGCTATGTCTCAAGAATGCGAAGTGGCCGCCYGTACACCTGCTCCAGGCTGTGACAAATCCATAAA.....T.....C.....G.....	4770 4770 4770
Consensus BDV JCT BDV Briese	ARAATGCGAGAGCTGGGCCGCTGAGCCCCGGYRTTTGACCGAGGATGGCAGCTCTTCGMAAGGTTGTTCATTCTAAGAATTGTGACC .G.....TG.....CA.....A..... .A.....	4860 4860 4860
Consensus BDV JCT BDV Briese	TAGATATGGATCCCGACTTCAACGATATTGTTAGCGAYAAGGCGATAATCAGCTCAAGAAGGACTGGGTATTYAGTACAAATGCAGCRGC.....T.....A.....G.....	4950 4950 4950

FIG. 2G

Consensus	CCTTTTGAAGAAATACRGTCARCGGTTGGAGAGGCCCYCCTGCCAGRTCGGAGCCTCACGRCTTGTGAATGCTCTRATCGATGGAGCCT	5040
BDV JCTA...G.....A...G.....A...A...A...G.....G.....	5040
BDV BrieseG...A.....A.....T.....G.....G.....A.....A.....	5040
Consensus	TAGAYAAATATCCAGCCCTGCTAGAGCCATTTTACAGGGGAGCGTTGAGTTYGAGGATCGGYTGACTGTGCTGCTGCCTAAGGAGAARG	5130
BDV JCT	...T.....C.....T.....C.....T.....C.....T.....C.....	5130
BDV BrieseC.....C.....C.....T.....C.....T.....A.....A.....	5130
Consensus	AGTTRAAGGTAAGGCAAGGTTCTTCTCGAAGCAACATTTGGCAATCAGGATATATACAGTTGTGCTGAAGCTGCACCTTAAGAAAYGAGG	5220
BDV JCT	...G.....A.....A.....A.....A.....A.....A.....A.....	5220
BDV BrieseA.....A.....A.....A.....A.....A.....A.....T.....	5220
Consensus	TTATGCCATACYTAAARACACAYTCAATGACCATGAGCTCAACGGCYCTAACYCAYCTTCTTAACGGGCTATCACATATCATCATCAAGG	5310
BDV JCTT...A...T...C.....C.....C...T.....C.....C.....	5310
BDV BrieseC...G...C.....C.....T...T...C.....T...C.....	5310
Consensus	GTGACTCCTTTGTATTAAACYTWGAYTATAGYTCCTGGTGCAACGGTTCCGACCAAGCACTRCARGCCCCCANTCTGTGTCGTCAGTTGGATC	5400
BDV JCTT.A..T...C.....C.....A.....A.....C.....	5400
BDV BrieseC.T..C...T.....T.....G...G...A.....A.....	5400
Consensus	AGATGTTCAATTGCGGGTACTTCTTCAGGACTGGGTGCACACTGCCATGCTTTACCAGTTTATTATTCARGACAGRTTCAACCCGCCCT	5490
BDV JCTA.....A.....A.....A.....A.....A.....A.....	5490
BDV BrieseA.....A.....A.....A.....A.....A.....G.....	5490
Consensus	ATTCCYTCMGTGTGAGCCCGTTGAAGACGGWGYACATGCCGGTTGGGACTAARACAATGGGRGAGGGYATGAGGCAGAAAACATATGA	5580
BDV JCTT..C.....T..C.....T..C.....A.....T.....G.....	5580
BDV BrieseC..A.....A..T.....A.....G.....C.....C.....	5580
Consensus	CAATYCTTACGAGCTGCTGGGAGATAATTGCTCTTCGGGAAATTAAACGTGACGTTTAAATATACTAGGCCARGGTGATATATCAGACAATCA	5670
BDV JCTT.....T.....T.....T.....T.....T.....G.....	5670
BDV BrieseC.....C.....C.....C.....C.....C.....A.....	5670

FIG. 2H

Consensus	TYRTACATAAATCTGCAAGCCCAAAATAAYCAGCTATTAGCGGAGCGAGCAYTRGGRGCTYTTGTACAGCATGCTAGATTAGCTGGCCATA	5760
BDV JCT	.TG.....T.....T.....T.G..A..TT.....	5760
BDV Briese	.CA.....C.....C.A..G..CC.....	5760
Consensus	ACCTYAAGGTAGARGAATGYTGGGTGCAGATTGTCTGTATGATGGAAGAAGCTYTTCTTCCTGGGTACCTGTCCCRGGCTGTT	5850
BDV JCTT.....A.....T.....C.....C.....A.....	5850
BDV BrieseC.....G.....C.....T.....T.....G.....	5850
Consensus	TGAAGCAGCTCTCRCGGGTGACGGGAYTCYACTGGRGAGYTATTCCCAAACCTATACTCAAAGTTAGCCTGCTTAACATCATCRTCYTAA	5940
BDV JCTG.....C.....C.....G..T.....	5940
BDV BrieseA.....T..T.....A..C.....	5940
Consensus	GCGCAGCGATGGCAGACACATCYCCATGGGTGGCACTCGCGACAGGTGTCTGTCTGTATCTTATCGAGTTRTATGTTGAGCTGCCCTCCRG	6030
BDV JCTC.....T.....	6030
BDV BrieseG.....A.....	6030
Consensus	CAATCAGCAGGAYGAGTCGGCTRTTRACGACCCCTCTGYCTCGTAGGYCCATCCATTGGTGGGCTTCACACCTGCAACCCCTRCCCAGTG	6120
BDV JCTC.....G..A.....T.....T.....A..T.....G.....	6120
BDV BrieseT.....A..G.....C.....C.....G..C.....A.....	6120
Consensus	TCTTTTTCAGAGGAATGTCGAGACCCAYTGCCCTTTCAGCTAGCACTCTTGCAGACCCCTCATTAARACGACAGGGGTGACVYGTGAGCTGG	6210
BDV JCTT.....C.....	6210
BDV BrieseG.....	6210
Consensus	TGAATCGTGTGTGTYAAGTTACGGATAGCACCCCTATCCAGACTGGCTCTCYCTAGTGTGACTGACCCGACVTCACCTCAACATGTCYCARGTGT	6300
BDV JCTT.....C.....G..A.....C.....T.....T.....G.....	6300
BDV BrieseC.....T.....C.....C.....A.....	6300
Consensus	ACCGCCAGAACGTCARATCAGGAGGTGGATTGAGGARGCRATAGCRACAAGCTCACACTCGTCACGCATAGCAACTTYYTTCACGAGS	6390
BDV JCTA.....G..A.....G..A.....A.....T.....G.....	6390
BDV BrieseG.....A..G.....G.....C.....C.....C.....	6390

FIG. 21

Consensus	CCCTCAGGAGATGGCYCAGYTGCTTGCAGGAGCACCTYTCAACAATGATGCCTCTTCGRCCCGGGGATATGTGGCCTTATTTCGCATTAT	6480
BDV JCTC...C.....C.....G.....	6480
BDV BrieseT...T.....T.....A.....	6480
Consensus	CAAATGTCGCATAYGGTYTAAGCATATAGATCTATTTCAAAARTCCCTCTACCGTTGTYTCTGCAAGTCAAGCTGTCATATCGARGATG	6570
BDV JCTT...C.....G.....C.....A....	6570
BDV BrieseC...T.....A.....T.....G....	6570
Consensus	TTGCCCTAGAGAGTGTAAGGTATAAGGAATCTATCATYCAAGGCTCTGTAGACACYACTGAGGGGTAYAACATGCAACCTTATTTGGAAG	6660
BDV JCTT.....C.....T.....C.....T.....	6660
BDV BrieseC.....C.....C.....T.....	6660
Consensus	GTTGCACCTTACCTTGCAGCCCAARCAGYTACGKAGGTTGACRTGGGGTCGAGACCTAGTTGGAGTYACATGCCGTTGTGCCGAGCAAT	6750
BDV JCTG...C...G.....G.....T.....	6750
BDV BrieseA...T...T.....A.....C.....C.....	6750
Consensus	TCCATCCYCAYAGTTCTGTSGTSCAAARGCRGAACCTCTACCTCGAYCTATYATATACTCCCCACARGAGACRWTGCCGTCACACCATC	6840
BDV JCTC..T.....C.....A..A.....T...C.....A...G.....	6840
BDV BrieseT..C.....G.....G...G.....C...T.....G...A.....	6840
Consensus	TGACTACCAGGGGGACCCGCTTTACCTYGGATCYAATACGGCTGTCCAMGGTYCAGCGAGGTGAGATCACRGGCCTAACAAAGTCAA	6930
BDV JCTT.....T.....C...T.....C...T.....A.....G.....	6930
BDV BrieseC.....C.....A...C.....G.....	6930
Consensus	GGGCTGCAAAATCTAGTCARGGACACTCTCGTTCTCCAYCAGTGGTYAARGTCCGTAARGTTACCGATCCACACTGAACACYCTCATGG	7020
BDV JCTA.....G.....C.....C...G.....G.....T.....	7020
BDV BrieseG.....T.....T...A.....A.....C.....C.....	7020
Consensus	CRCGCTTCTTRCTTGAGAAGGGTACACATCTGACGCTCGRCCTAGCATYCAGGGTGGGACCCTCACRCATCGTCTCCATCCCGYGGAG	7110
BDV JCT	.G.....G.....A.....G.....T.....A.....A.....T....	7110
BDV Briese	.A.....A.....G.....A.....C.....G.....G.....C.....	7110

FIG. 2J

Consensus	ACTCAGSCARGGGCTYACTGGGTATGTRAAATATACTAMAGYACGTGGCTYCGRTTCTCAAGTGATTATCTTCACTCTTTCTCGAAATCAT	7200
BDV JCTC..A.....C.....G.....C..C.....C..G.....	7200
BDV BrieseG..G.....T.....A.....A..T.....T..A.....	7200
Consensus	CAGAYGACTAYACAATCCACTYACGATGTATTACATACGGTTGCCCTCTATGCTGATTCCGGTGATTAGATCGGGCGGTGTATTTC	7290
BDV JCTT.....C.....C.....	7290
BDV BrieseC.....T.....	7290
Consensus	CTCCTTACCTTTTGAGTGCAAGTTGTAAACATGCTTTGAGAAGATAGACTCAGAGGAGKTCGTCCTGGCATGYGAACCYCAATAYAGGG	7380
BDV JCT	7380
BDV Briese	7380
Consensus	GTGCTGACTGGCTGATATCAAGCCAGTYACTGTCCCTGAGCAGATAAYTGAYGCTGAAGTCGAGTTTGACCCCTGTGTGAGTCGGRGTT	7470
BDV JCTT.....T.....T..C.....	7470
BDV BrieseC.....C.....T.....	7470
Consensus	ATTGTCFCGGGATTCTCATTTGGCAAGTCATTCCTTRGTTGACATTAAGGGCAAGTGGGATGATATYATGGAGCACGGGACATGGGGCTAAC	7560
BDV JCTG.....A.....	7560
BDV BrieseA.....A.....C.....	7560
Consensus	TGGAGAGGTTTCTGTRTCGGACATGCAGAAACTTCCTRTGGAGTATTGTAAATTCGGTCTCTCTGGAGATTCCCTATTGGCGCACGRCTCC	7650
BDV JCTG.....A.....	7650
BDV BrieseA.....G.....	7650
Consensus	TYCAGTTTGAGAAGGCTGGCCTYATTAGRATGCTGTATGCTGCRACAGGTCCAACCCYTAGCTTCCTAATGAAGTYTTTCAAGACTCAG	7740
BDV JCT	.C.....T.....G.....A.....TT.....C.....	7740
BDV Briese	.T.....C.....A.....G.....CC.....T.....	7740
Consensus	CCCTMCTYATGGACTGGGACCCYCTYATCGGCTGTGCCCTAGATCAACTTTCATAGTCGGGAGACCTCGTYGCTYAGCTYGTATTAT	7830
BDV JCTA..T.....T..T.....A.....C.....C.....C.....	7830
BDV BrieseC..C.....C..C.....C.....T..T.....T.....	7830

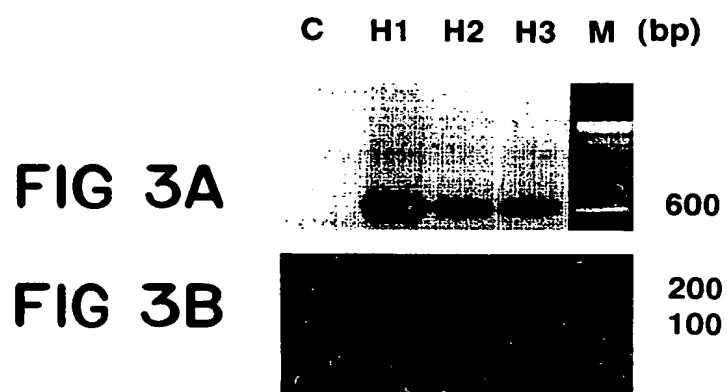
FIG. 2K

Consensus	TRCCCTTCATCAACCCGGGTATAGTGGAGATTGAAGTGTCTRGAATTAATAGCAAGTAYCATGCAGTATCGGAGGCYAAATATGGATCTGT	7920
BDV JCT	.A.....A.....A.....T.....T.....	7920
BDV Briese	.G.....G.....C.....C.....	7920
Consensus	ACATCGCTGCTGCMARCTCTGTGGCGTAAAGCCACACAGTTTGTGTGAGAAACAACGACTTTACGGCCGCGGCCACCATGGTT	8010
BDV JCTA..A.....A.....	8010
BDV BrieseC..G.....G.....	8010
Consensus	GTTATTCCTTCTTGGTCTAAGTCACGCAATCAATCACAGTCTCTAAGATGGTAGTRCGGAAGCTGAAGCTMTGTCTCTGTATATAT	8100
BDV JCT	8100
BDV BrieseA.....A.....C.....	8100
Consensus	ACCCACAGTCGATCCCGCGGTGCTCTCGACCTGTGCCAYCTRCCAGCAYTAACATAATCCTAGTGTCTCGGCGGTGACCCAGCGTACT	8190
BDV JCTC..G.....C.....T.....	8190
BDV BrieseT..A.....T.....	8190
Consensus	AYGAGCGATTACTTGAGATGGACCTRTGCGGGGCTGTGTCAAGTCGMPYGATATCCCCATTTCYCTRGCTGSCAGAACGCACAGGGGT	8280
BDV JCT	.C.....A.....C..T.....C..A.....C.....	8280
BDV Briese	.T.....G.....A..C.....T..G.....G.....	8280
Consensus	TCCARTRGCCCGACGCTGGTCCAGGTGTRATTAGACTYGACARGTTAGAGTCTCRGTTTGTATTAYGCYACCCCTGTTTRGAGGARCTAG	8370
BDV JCT	..A..A.A.....G.....T..A.....G.....C..C.....G.....G.....	8370
BDV Briese	..G..G.G.....A.....C..G.....A.....T..T.....A.....A....	8370
Consensus	AGTTTAATGCTAYCTAGACTCTGAGTTRGTTGAYATTAGTGATATGTGCTGCCCTCCCYTAGCGACACCCTGTAGGCCCTWTCAGGC	8460
BDV JCTG..C.....A.....T.....C.....A.....	8460
BDV BrieseA..T.....G.....C.....T.....T.....T.....	8460
Consensus	CARTRATCGGAGCTTACAGTCGTTTCAGGTAGCCTTAATGGACAACATATAGTTTGTMTAGGACCTCATYATCCGGRGGRSTGGACA	8550
BDV JCT	..G.G.....	8550
BDV Briese	..A.A.....C.....C.....T.....A..AC.....	8550

FIG. 2L

Consensus	TYAGGCCCTCAGGARTTTGAYGARTGCTTGTGGTRGGRCAGCAYATCCTCGGYCAGCCCCGTCCCTAGTRGAGGTTGTTTACTACG	8640
BDV JCT	.C.....G.....T..A.....G..G.....T.....T.....G.....G.....	8640
BDV Briese	.T.....A.....C..G.....A.....A.....C.....C.....A.....G.....	8640
Consensus	TTGGAGTTGTRGGAAGCGYCCTGCTGTAGCGAGGCATCCSTGGTCAGCAGATCTTAAGCGAATYACTGTRGGGGGCGRGCKCCCTGCC	8730
BDV JCTG.....T.....C.....C.....C.....C.....A.....A.....G.....	8730
BDV BrieseA.....C.....G.....T.....G.....G.....G.....T.....	8730
Consensus	CYTCTGCTGCGYRGAYTGGGTGATGAGGATTGTCRGGGGTCTCTGYTGGTTGGGCTCCYGGCTGGRTTGACGCAGTTTGTGRTTGTGATT	8820
BDV JCT	.T.....TG..C.....G.....C.....C.....A.....G.....G.....G.....	8820
BDV Briese	.C.....CA..T.....A.....T.....T.....G.....A.....A.....A.....	8820
Consensus	RAGRTYRAGCCAYCTACTRCCCTATTCTTAAAAAACCATAYGTCAGTGGTGACGTGCTTGGGYTTGGTTGCTTTGTGTAGCGCKTT	8910
BDV JCT	G..G..TG.....T.....G.....C.....T.....T.....T.....T.....	8908
BDV Briese	A..A.CA.....C.....A.....T.....C.....G.....G.....G.....	8910

FIG. 2M



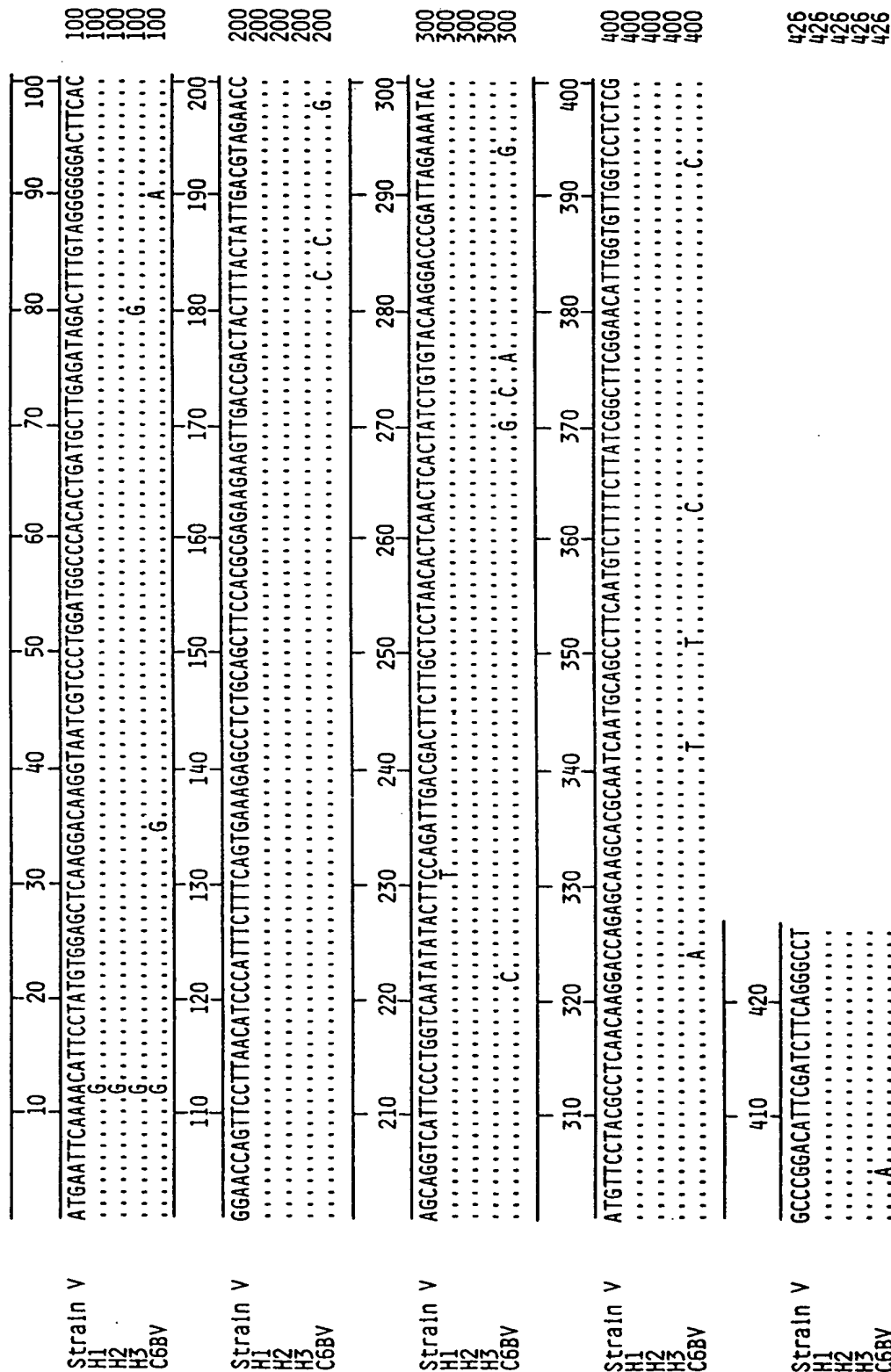
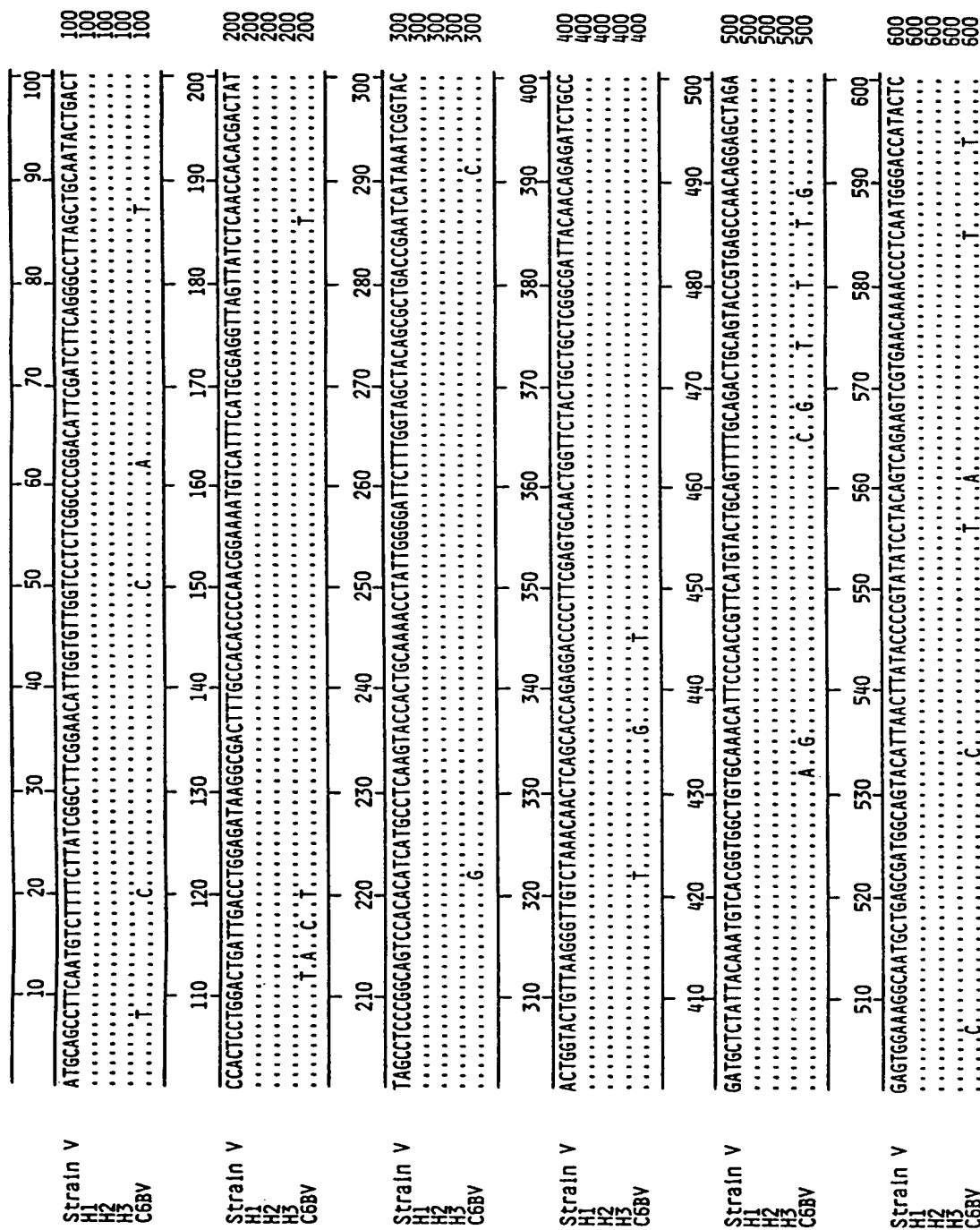


FIG. 4B



Strain V	610	620	630	640	650	660	670	680	690	700	700
H1	TGCACTCATCCTCTAAGATAGTTTCCTCGATGAATTAGCGGTTCATACCTCCCTAACGAATGGTAGTTACGAGGCTCATCAATCAATGTGACGTGTG										700
H2										700
H3										700
C6BVC.....			G.....						700
Strain V	710	720	730	740	750	760	770	780	790	800	800
H1	CAAACACGTCGTCTGCCGGCCCGAGGTTGAAAGCGCGGTAGGACACCCAGCAGATTGAGTATCTAGTTACAGGCTTAGGCCACACTGAAGA										800
H2										800
H3										800
C6BVT.....A.....G.....T.....T.....A.....C.....T.....			800
Strain V	810	820	830	840	850	860	870	880	890	900	900
H1	TGCATGGGAGGACTGTGAGATCCTCCAGTCTCTGCTCTAGGGGTGTTGGTACTGGGATCGCAAGTGCTTCTCAATTTTGAGGAGCTGGCTCAACCAC										900
H2										900
H3										900
C6BVG.....A.....T.....G.....C.....G.....					900
Strain V	910	920	930	940	950	960	970	980	990	1000	1000
H1	CCTGACATCATCGGGTATAGTTAATGGAGTTGGGTTGTCCTGGCATGCCATCGTGTATATGTACGTTACGCGTGGGAATGAGTCCACCTATTACC										1000
H2										1000
H3										1000
C6BVT.....A.....A.....T.....G.....C.....G.....A.....			1000
Strain V	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1100
H1	CTCCAGTAGATTACAATGGCGGAAGTACTTCTCGAATGATGAGGGAAGGTTACAACAACACCCCGAGGCAAGGCCAGGGCTTAAGCGGTCATGTG										1100
H2										1100
H3										1100
C6BVA.....T.....G.....C.....							1100
Strain V	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1200
H1	GTTCCGAGGTACTTCTAGGACAGTAGGGTCTGGGGTGAACCCAGGAGGATTCGGTACAATAAGACCTCACATGACTACCACCTGGAGGAGTTTGAG										1200
H2										1200
H3										1200
C6BVT.....T.....T.....T.....A.....		1200

FIG. 4C-2

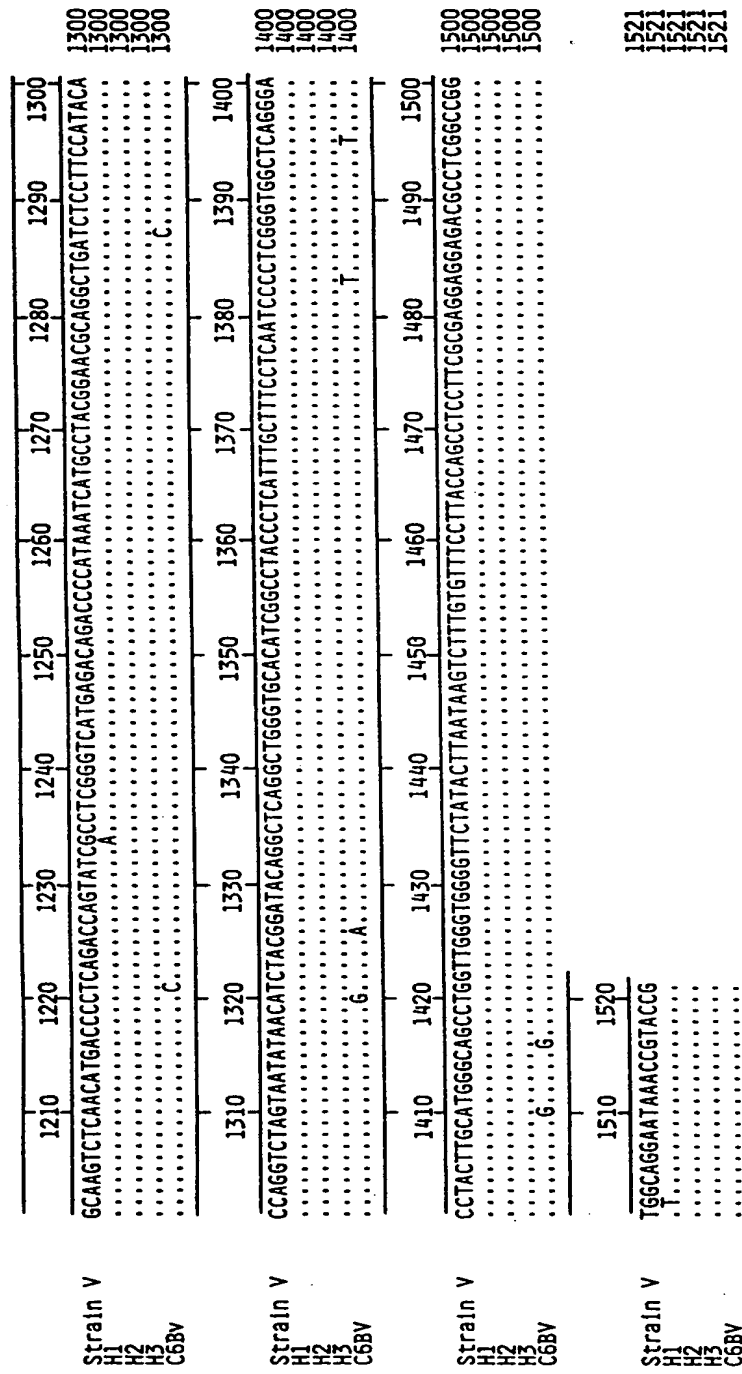


FIG. 4C-3

C6BV p40Int	50	
H1 p40Int	50	
H2 p40Int	50	
H3 p40Int	50	
StrainV p40Int	50	
Consensus	TTCA	YACAGT	AACGCC	YAGC	CTTGTGTTTC	TATGTTTGCT	AATCCCAGGA	50	
C6BV p40Int	100	
H1 p40Int	100	
H2 p40Int	100	
H3 p40Int	100	
StrainV p40Int	100	
Consensus	CTGCACGCTG	CGTTTGTTCA	CGGAGGGGTG	CCTCGTGAAT	Y	TACCTGTC		100	
C6BV p40Int	150	
H1 p40Int	150	
H2 p40Int	150	
H3 p40Int	150	
StrainV p40Int	150	
Consensus	GACGCCT	RTTY	ACGCGTG	GRG	AACAGACTGT	YGTTAAGACT	GRRAGTTTT	150	
C6BV p40Int	200	
H1 p40Int	200	
H2 p40Int	200	
H3 p40Int	200	
StrainV p40Int	200	
Consensus	ACGGGGAAAA	GAC	RA	RCAG	CGTGATCTCA	CCGAGCTGGA	GATCTCCTCT	200	
C6BV p40Int	250	
H1 p40Int	250	
H2 p40Int	250	
H3 p40Int	250	
StrainV p40Int	250	
Consensus	AT	TT	CAGCC	ATTGTTGCTC	ATTACTAAT	W	GGGGTTGTGA	TAGGATCGTC	250
C6BV p40Int	300	
H1 p40Int	300	
H2 p40Int	300	
H3 p40Int	300	
StrainV p40Int	300	
Consensus	RTCTAAGATY	AAAGCAG	RAG	CCGAGCAGAT	CAAGAAAAGG	TTTAAACTA		300	

FIG. 5A-I

C6BV p40IntT.....T	350
H1 p40IntT.....C	350
H2 p40IntG.....C	350
H3 p40IntT.....C	350
StrainV p40IntT.....C	350
Consensus	TGATGGCAGC CKTAAACCGG CCATCCCATG GTGAGACTGC TACACTACTY	350
C6BV p40IntG.....	400
H1 p40IntA.....	400
H2 p40IntA.....	400
H3 p40IntA.....	400
StrainV p40IntA.....	400
Consensus	CAGATGTTTA ATCCACATGA GGCTATAGAT TGGATTAACG GCCARCCCTG	400
C6BV p40IntT.....	450
H1 p40IntC.....	450
H2 p40IntT.....	450
H3 p40IntT.....	450
StrainV p40IntT.....	450
Consensus	GGTAGGCTCC TTTGTGTTGY CTCTACTAAC TACAGACTTT GAGTCCCCAG	450
C6BV p40IntC.....A.....G.....	500
H1 p40IntT.....C.....G.....	500
H2 p40IntT.....C.....G.....	500
H3 p40IntT.....C.....G.....	500
StrainV p40IntT.....C.....G.....	500
Consensus	GTAAAGAATT YATGGAYCAG ATTAARCTTG TCGCAAGTTA TGORCAGATG	500
C6BV p40IntT.....	550
H1 p40IntC.....	550
H2 p40IntC.....	550
H3 p40IntC.....	550
StrainV p40IntC.....	550
Consensus	ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGYA TGGATGCTAC	550
C6BV p40IntT.....	571
H1 p40IntT.....	571
H2 p40IntT.....	571
H3 p40IntT.....	571
StrainV p40IntC.....	571
Consensus	CCTTACAATC CCYGTAGTTG C	571

FIG. 5A-2

Consensus	TGACCATGAG CTCAACGGGY CTAAGCAYC TTCTTAACCG GCTATCACAT	50
p180fragC.....C.....T.....	50
H1 p180T.....T.....C.....	50
H2 p180T.....T.....C.....	50
H3 p180T.....T.....C.....	50
Strain 5 p180T.....T.....C.....	50
Consensus	ACTATCACTA AGGGTGACTC CTTTGTATT AAQYMGAYI ATAGTCCTG	100
p180fragT.....A.....T.....C.....	100
H1 p180C.....T.....C.....T.....	100
H2 p180C.....T.....C.....T.....	100
H3 p180C.....T.....C.....T.....	100
Strain 5 p180C.....T.....C.....T.....	100
Consensus	GTGCAACGGT TTCCGACCAG AACTRCARGC CCCAMTCTGT CGTCAGTTGG	150
p180fragA.....A.....C.....	150
H1 p180G.....G.....A.....	150
H2 p180G.....G.....A.....	150
H3 p180G.....G.....A.....	150
Strain 5 p180G.....G.....A.....	150
Consensus	ATCAGATGTT CAATTGCGGG TACTTCTTCA GGACTGGGTG CACACTGCCA	200
p180frag	200
H1 p180	200
H2 p180	200
H3 p180	200
Strain 5 p180	200
Consensus	TGCTTTACCA CGTTTATTAT TCARGACAGR TTCAACCCGC CCTATTCQYI	250
p180fragG.....A.....T.....	250
H1 p180A.....G.....C.....	250
H2 p180A.....G.....C.....	250
H3 p180A.....G.....C.....	250
Strain 5 p180A.....G.....C.....	250
Consensus	GTGGTGAG CCCGTTGAAG ACGGMYAC ATGCGCGGT GGGACTAARA	300
p180fragC.....T.....C.....G.....	300
H1 p180A.....A.....T.....A.....	300
H2 p180A.....A.....T.....A.....	300
H3 p180A.....A.....T.....A.....	300
Strain 5 p180A.....A.....T.....A.....	300

FIG. 5B-I

Consensus	CAATGGGGA GGGATGAGG CAGAACTAT GGACAATCT TACGAGCTGC	350
p180fragA.....T.....T.....	350
H1 p180G.....C.....	350
H2 p180G.....C.....	350
H3 p180G.....C.....	350
Strain 5 p180G.....C.....	350
Consensus	TGGGAGATAA TTGCTCTTCG GGAAATTAAC GTGACGTTA ATATACTAGG	400
p180fragT.....	400
H1 p180C.....	400
H2 p180C.....	400
H3 p180C.....	400
Strain 5 p180C.....	400
Consensus	CCARGGTGAT AATCAGACAA TCATYRTACA TAAATCTGCA AGCCAAAATA	450
p180frag	...G.....TG.....	450
H1 p180	...A.....CA.....	450
H2 p180	...A.....CA.....	450
H3 p180	...A.....CA.....	450
Strain 5 p180	...A.....CA.....	450
Consensus	ATCAGCTATT AGCGGAGCGA GCATTTGGGG GYTTGTACAA GCATGCTAGA	500
p180frag	..T.....T..G..A..TT.....	500
H1 p180	..C.....C..A..G..CC.....	500
H2 p180	..C.....C..A..G..CC.....	500
H3 p180	..C.....C..A..G..CC.....	500
Strain 5 p180	..C.....C..A..G..CC.....	500
Consensus	TTAGCTGGCC ATAACCTTAA GGTAGARGAA TGTGGGTGT CAGATTGTCT	550
p180fragT.....A.....T.....	550
H1 p180C.....G.....C.....	550
H2 p180C.....G.....C.....	550
H3 p180C.....G.....C.....	550
Strain 5 p180C.....G.....C.....	550
Consensus	GTATGAGTAT GGAAAGAAGC TTTCTTCCG TGGTGTACCT GTCCGAGGCT	600
p180fragC.....A.....	600
H1 p180T.....G.....	600
H2 p180T.....G.....	600
H3 p180T.....G.....	600
Strain 5 p180T.....G.....	600

FIG. 5B-2

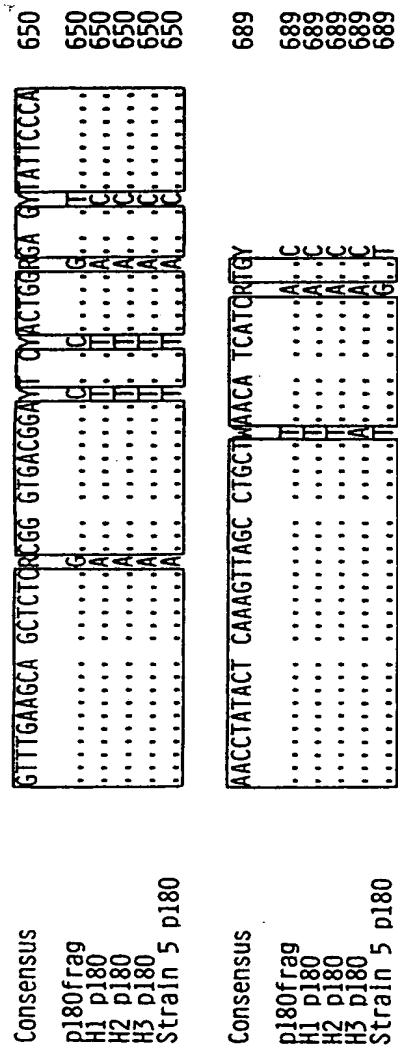


FIG. 5B-3

	p24					p16			p56															
	4	26	34	127	194	12	27	108	3	7	17	21	220	234	242	243	245	282	296	326	412	465	501	
C6BV	G	S	I	H	A		G	D	E	L	S	A	Q	A	V	S	L	R	M	G	A	A	L	W
H1	E	-	V	Y	T		D	-	D	P	F	V	R	T	A	P	R	L	V	S	T	T	P	L
H2	-	-	V	-	T		-	-	D	P	F	V	R	T	A	P	R	L	V	S	T	-	P	-
H3	E	-	V	-	T		-	G	D	P	F	V	R	T	A	P	R	L	V	S	T	-	P	-
Strain V	R	P	V	-	T		D	-	D	P	F	V	R	T	A	P	R	L	V	S	-	-	P	-

FIG. 6A

p24						p16					p56						
	C6BV	H1	H2	H3	Strain V		C6BV	H1	H2	H3	Strain V		C6BV	H1	H2	H3	Strain V
C6BV		16	14	14	17			17	16	17	16			67	65	65	64
H1	4	2	1		5		2		2	3	3		15		2	2	3
H2	2	2	2	2	3		1	1		1	1		13	2		0	1
H3	3	1	1		5		2	2	1		2		13	2	0		1
Strain V	4	3	2	2			1	1	0	1			12	3	1	1	

FIG. 6B

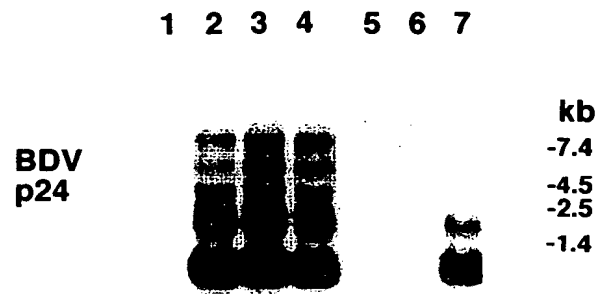


FIG. 7A

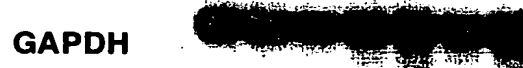
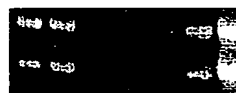


FIG. 7B



1 2 3 4 5 6 7

FIG. 7C

MATEPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPRNALTQVDQQLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDYSDSIRILGENIKILDRSMKTMETMKLMMKEKVDLLYASTAVGTSAPMLPSHP
APPRIYPQLPSAPTDEWDIIP

FIG. 8A

MATGPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPRNALTQVDQQLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDHSDSIRILGENIKILDRSMKTMETMKLMMKEKVDLLYASTAVGTSAPMLPSHP
APPRIYPQLPSAPTDEWDIIP

FIG. 8B

MATEPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPRNALTQVDQQLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDHSDSIRILGENIKILDRSMKTMETMKLMMKEKVDLLYASTAVGTSAPMLPSHP
APPRIYPQLPSAPTDEWDIIP

FIG. 8C

MNSKHSYVELKDKVIVPGWPTLMLEIDFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLLTLSLSVYKDPIRKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9A

MNSKHSYVELKDKVIVPGWPTLMLEIDFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLLTLSLSVYKDPIRKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9B

MNSKHSYVELKDKVIVPGWPTLMLEIGFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLLTLSLSVYKDPIRKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9C

MQPSMSFLIGFGTLVLVLSARTFDLQGLSCNTDSTPGLIDLEIRRLCHTPTENVISCEVSYL
NHTTISLPAVHTSCLKYHCKTYWGFFGSYADRINRYTGTVKGCLNNSAPEDPFECNW
FYCCSAITTEICRCSITNVTVAVQTFPPFMYCSFADCS TVSQELES GKAMLS DGGSTLTYT
PYILQSEVVNKTILNGTILCNSSSKIVSFDEFRRSYSLTNGSYQSSINVT CANYTSSCRPRL
KRRRRDTQIEYLVHKLRLKDAWEDCEILQSLLLGVFGTGIASASQFLRSWLNHPDII
GYVNGVGVVWQCHRVNVTFMTWNESTYPPVDYNGRKYFLNDEGR LQTNTPEARPG
LKRVMWFGRYFLGT V GSGVKPRRIRYNKTSHDYHLEEF EASLNMTPQTSITSGHETDPI
NHA YGTQADLLPYTRSSNITSDTGS GWVHIGLPSFAFLNPLGWLRD LLA WAAWLGGV
LYLISLCVSLPASFAARRRLGRLQE

FIG. 10A

MQPSMSFLIGFGTLVLVLSARTFDLQGLSCNTDSTPGLIDLEIRRLCHTPTENVISCEVSYL
NHTTISLPAVHTSCLKYHCKTYWGFFGSYADRINRYTGTVKGCLNNSAPEDPFECNW
FYCCSAITTEICRCSITNVTVAVQTFPPFMYCSFADCS TVSQELES GKAMLS DGGSTLTYT
PYILQSEVVNKTILNGTILCNSSSKIVSFDEFRRSYSLTNGSYQSSINVT CANYTSSCRPRL
KRRRRDTQIEYLVHKLRLKDAWEDCEILQSLLLGVFGTGIASASQFLRSWLNHPDII
GYVNGVGVVWQCHRVNVTFMTWNESTYPPVDYNGRKYFLNDEGR LQTNTPEARPG
LKRVMWFGRYFLGT V GSGVKPRRIRYNKTSHDYHLEEF EASLNMTPQTSITSGHETDPI
NHA YGTQADLLPYTRSSNITSDTGS GWVHIGLPSFAFLNPLGWLRD LLA WAAWLGGV
LYLISLCVSLPASFAARRRLGRWQE

FIG. 10B

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTPSLVFL	CLLIPGLHAA	FVHGVVPRES	YLSPTPIRGE	QIVVKTAKFY
GEKTIQRDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKKRFKIM
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGSEFVLP	LLTTDFESPG
KEFMDQIKLV	ASYAQMTITYT	TIKEYLAECM	DATLTIPW	

FIG. IIA

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTPSLVFL	CLLIPGLHAA	FVHGVVPRES	YLSPTPIRGE	QIVVKTAKFY
GEKTIQRDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAEA	EQIKKRFKIM
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGSEFVLS	LLTTDFESPG
KEFMDQIKLV	ASYAQMTITYT	TIKEYLAECM	DATLTIPW	

FIG. IIB

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTPSLVFL	CLLIPGLHAA	FVHGVVPRES	YLSPTPIRGE	QIVVKTAKFY
GEKTIQRDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKKRFKIM
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGSEFVLS	LLTTDFESPG
KEFMDQIKLV	ASYAQMTITYT	TIKEYLAECM	DATLTIPW	

FIG. IIC

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
TMSSTAL/HL	LNRLSHITIK	GDSFVINLDY	SSWNGFRPE	LQAPICRQLD
QMFNGYFFR	TGCTLPCFTT	FLIQDRENPP	YSLSGEPVED	GVICAVGIKT
MGEGRQKLW	TLITSCWEII	ALREINVTFN	ILQGEDNQTI	IHKASQNN
QLLAERALGA	LYKHARLAGH	NLKVEECOWS	DCLYEYGGKL	FFRGVPVPGC
LKQLSRVIDS	TGELFRNLYS	KLCLTSSC		

50
100
150
200
229

FIG. 12